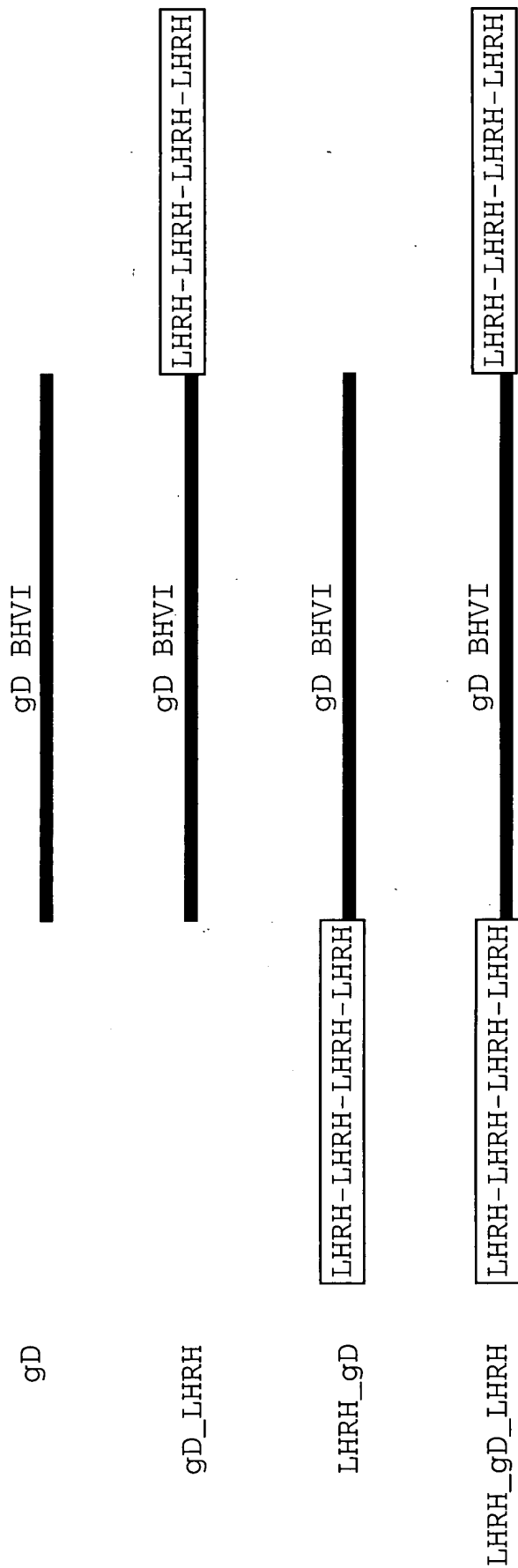


FIG. 1



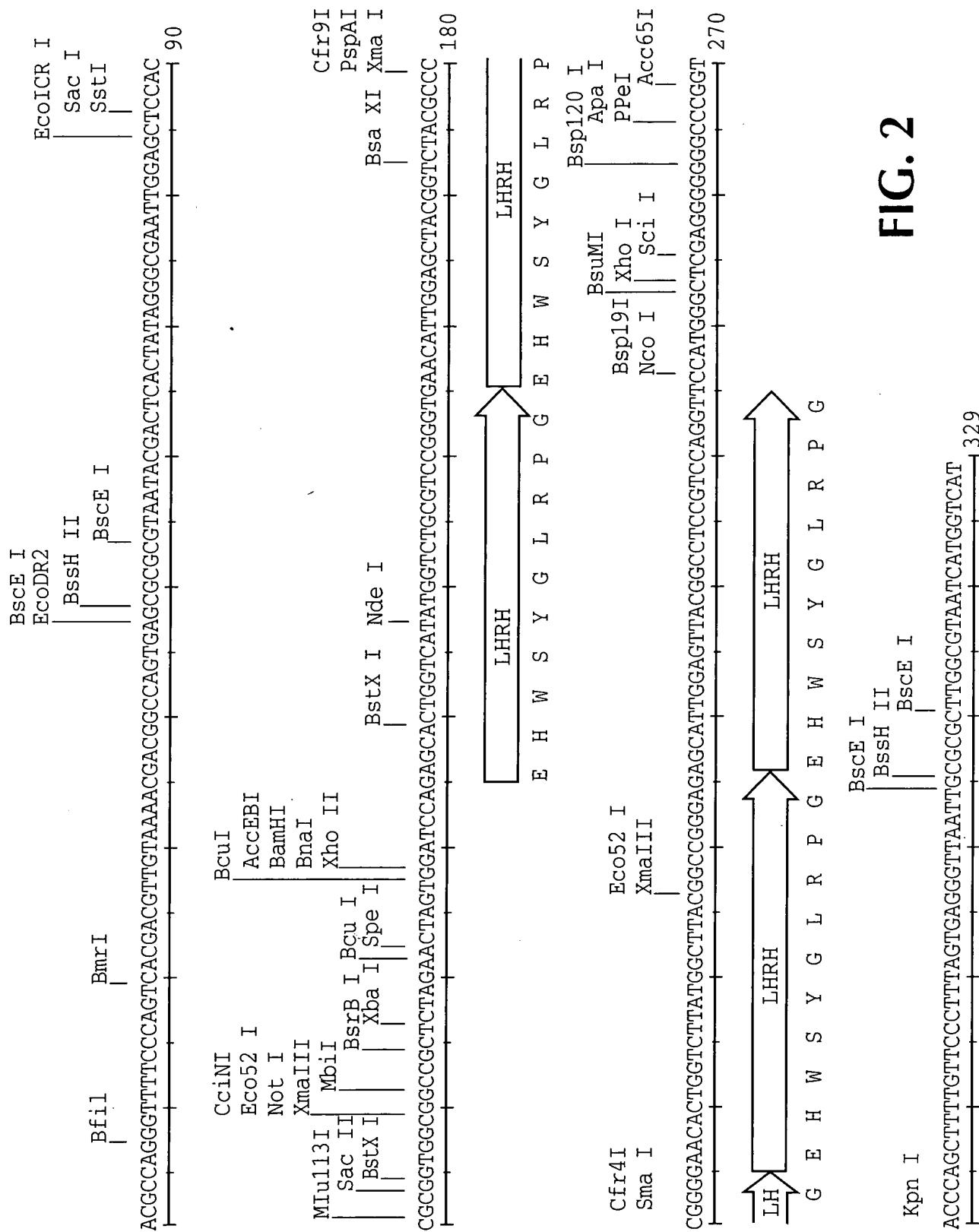


FIG. 2

FIG. 3B

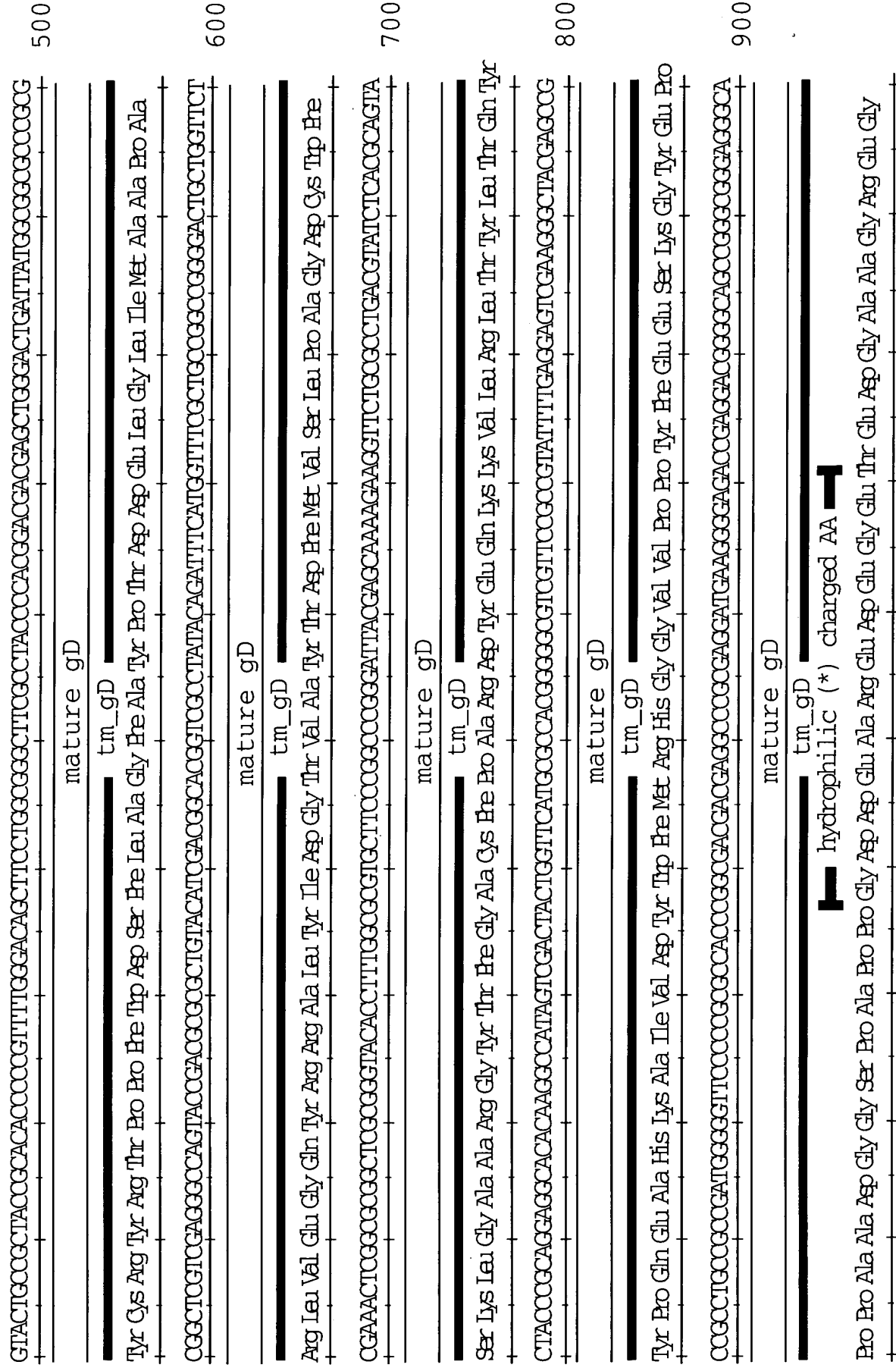


FIG. 4A

		10	20	30	40
1	ATG	G	A	G	GGGCCGACATTGGCCGTGCTGGGGCGCGCTGCTCG
1	ATG	CAAGGGCCGACATTGGCCGTGCTGGGGCGCGCTGCTCG			
		50	60	70	80
41	CCGTTGCGGT	A	AGCTTGCC	TACACCCGCGCCGCGGGTGAC	
41	CCGTTGCGGT	GAGCTTGCC	TACACCCGCGCCGCGGGTGAC		
		90	100	110	120
81	GGTATACGT	CGACCCGCGCGGTACCCGAT	TGCCGCGATAC		
81	GGTATACGT	CGACCCGCGCGGTACCCGAT	TGCCGCGATAC		
		130	140	150	160
121	AACTACACT	GAA	CGCTGGC	CACTACCGGGGCCCATACCGT	
121	AACTACACT	GAA	CGCTGGC	CACTACCGGGGCCCATACCGT	
		170	180	190	200
161	CGCCCTTC	GCAGACGGCCGCGAGCAGCCCGT	CGAGGTGCG		
161	CGCCCTTC	GCAGACGGCCGCGAGCAGCCCGT	CGAGGTGCG		
		210	220	230	240
201	CTACGCGAC	GAGCGCGGCGGCGTGCGACAT	TGCTGGCGCTG		
201	CTACGCGAC	GAGCGCGGCGGCGTGCGACAT	TGCTGGCGCTG		
		250	260	270	280
241	ATCGCAGAC	CCCGCAGGTGGGGCGCACGCTGT	TGGGAAGCGG		
241	ATCGCAGAC	CCCGCAGGTGGGGCGCACGCTGT	TGGGAAGCGG		
		290	300	310	320
281	TACGCCGGC	CACGCGCGCGGTACAACGCCACGGT	CATATG		
281	TACGCCGGC	CACGCGCGCGGTACAACGCCACGGT	CATATG		
		330	340	350	360
321	GTACAAGAT	CGAGAGCGGGTGCGCCCGGCCGCTGT	ACTAC		
321	GTACAAGAT	CGAGAGCGGGTGCGCCCGGCCGCTGT	ACTAC		
		370	380	390	400
361	ATGGAGTAC	ACCGAGTGCGAGCCCAAGCACTTT	GGGT		
361	ATGGAGTAC	ACCGAGTGCGAGCCCAAGCACTTT	GGGT		
		410	420	430	440
401	ACTGCCGCT	TACCGCACACCCCCGTTT	TGGGACAGCTTCCT		
401	ACTGCCGCT	TACCGCACACCCCCGTTT	TGGGACAGCTTCCT		

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FIG. 4B

	450	460	470	480
441	GGCGGGCTTCGCCTACCCACGGACGACGAGCTGGGACTG			
441	GGCGGGCTTCGCCTACCCACGGACGACGAGCTGGGACTG			
	490	500	510	520
481	ATTATGGCGGCGCCCGCGCGGCTCGTCGAGGGGCCAGTACC			
481	ATTATGGCGGCGCCCGCGCGGCTCGTCGAGGGGCCAGTACC			
	530	540	550	560
521	GACGCGCGCTGTACATCGACGGCACGGTCGCCTATACAGA			
521	GACGCGCGCTGTACATCGACGGCACGGTCGCCTATACAGA			
	570	580	590	600
561	TTTCATGGTTTCGCTGCCGGCCGGGGACTGCTGGTTCTCG			
561	TTTCATGGTTTCGCTGCCGGCCGGGGACTGCTGGTTCTCG			
	610	620	630	640
601	AAACTCGGCGCGGCTCGCGGGGTACACCTTTGGCGCGTGCT			
601	AAACTCGGCGCGGCTCGCGGGGTACACCTTTGGCGCGTGCT			
	650	660	670	680
641	TCCCGGCCCCGGGATTACGAGCAAAAGAAGGTTCTGCGCCT			
641	TCCCGGCCCCGGGATTACGAGCAAAAGAAGGTTCTGCGCCT			
	690	700	710	720
681	GACGTATCTCACGCAGTACTACCCGCAGGAGGCACACAAG			
681	GACGTATCTCACGCAGTACTACCCGCAGGAGGCACACAAG			
	730	740	750	760
721	GCCATAGTCGACTACTGGTTCATGCGCCACGGGGGCGTCG			
721	GCCATAGTCGACTACTGGTTCATGCGCCACGGGGGCGTCG			
	770	780	790	800
761	TTCCGCCGTATTTTGAGGAGTCGAAGGGGCTACGAGCCGCC			
761	TTCCGCCGTATTTTGAGGAGTCGAAGGGGCTACGAGCCGCC			
	810	820	830	840
801	GCCTGCCGCCGATGGGGGTTCCCCCGCGCCACCCGGGCGAC			
801	GCCTGCCGCCGATGGGGGTTCCCCCGCGCCACCCGGGCGAC			
	850	860	870	880
841	GACGAGGCCCGCGAGGATGAAGGGGAGACCGAGGACGGGG			
841	GACGAGGCCCGCGAGGATGAAGGGGAGACCGAGGACGGGG			

CGTGGTTCCTCG

[illegible]

+

FIG. 5

		10	20	30	40
1		MCGPTLAVLGALLAVAVSLPTPAPRVTVYVDPPAYPMPRY			
1		M[E]GPTLAVLGALLAVAVSLPTPAPRVTVYVDPPAYPMPRY			
		50	60	70	80
41		NYTERWHTTGPIPSPFADGREQPVEVRYATSAAACDMLAL			
41		NYTERWHTTGPIPSPFADGREQPVEVRYATSAAACDMLAL			
		90	100	110	120
81		IADPQVGRTLWEAVRRHARAYNATVIWYKIESGCARPLY			
81		IADPQVGRTLWEAVRRHARAYNATVIWYKIESGCARPLY			
		130	140	150	160
121		MEYTECEPRKHFGYCRYRTPPFWDSFLAGFAYPTDDELGL			
121		MEYTECEPRKHFGYCRYRTPPFWDSFLAGFAYPTDDELGL			
		170	180	190	200
161		IXAAPARLVEGQYRRALYIDGTVAYTDFMVSLPAGDCWFS			
161		IXAAPARLVEGQYRRALYIDGTVAYTDFMVSLPAFDCWFS			
		210	220	230	240
201		KLGAARGYTFGACFPARDYEQKKVLRLTYLTQYYPQEAHK			
201		KLGAARGYTFGACFPARDYEQKKVLRLTYLTQYYPQEAHK			
		250	260	270	280
241		AIVDYWFMRHGGVVPYPFEESKGYEPPPAADGGSPAPPGD			
241		AIVDYWFMRHGGVVPYPFEESKGYEPPPAADGGSPAPPGD			
		290	300	310	320
281		DEAREDEGETEDGAAGREGNGGPPGPEGDGESQTPEANGG			
281		DEAREDEGETEDGAAGREGNGGPPGPEGDGESQTPEANGG			
		330	340	350	360
321		AEGEPKPGPSPDADRPEGWPSLEAITHPPPAPATPA[-]APD			
321		AEGEPKPGPSPDADRPEGWPSLEAITHPPPAPATPAR[R]APD			
		370	380	390	400
360		AV[P]VSVGIGIAAAAIACVAAAAAGAYFVYTRRRGAGPLPR			
361		AV[S]VSVGIGIGIAAAAIACVAAAAAGAYFVY[I]RRRGAGPLPR			
		410			
400		KFKKLPAFGNVNYSALPG			
401		KFKKLPAFGNVNYSALPG			

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FIG. 6A

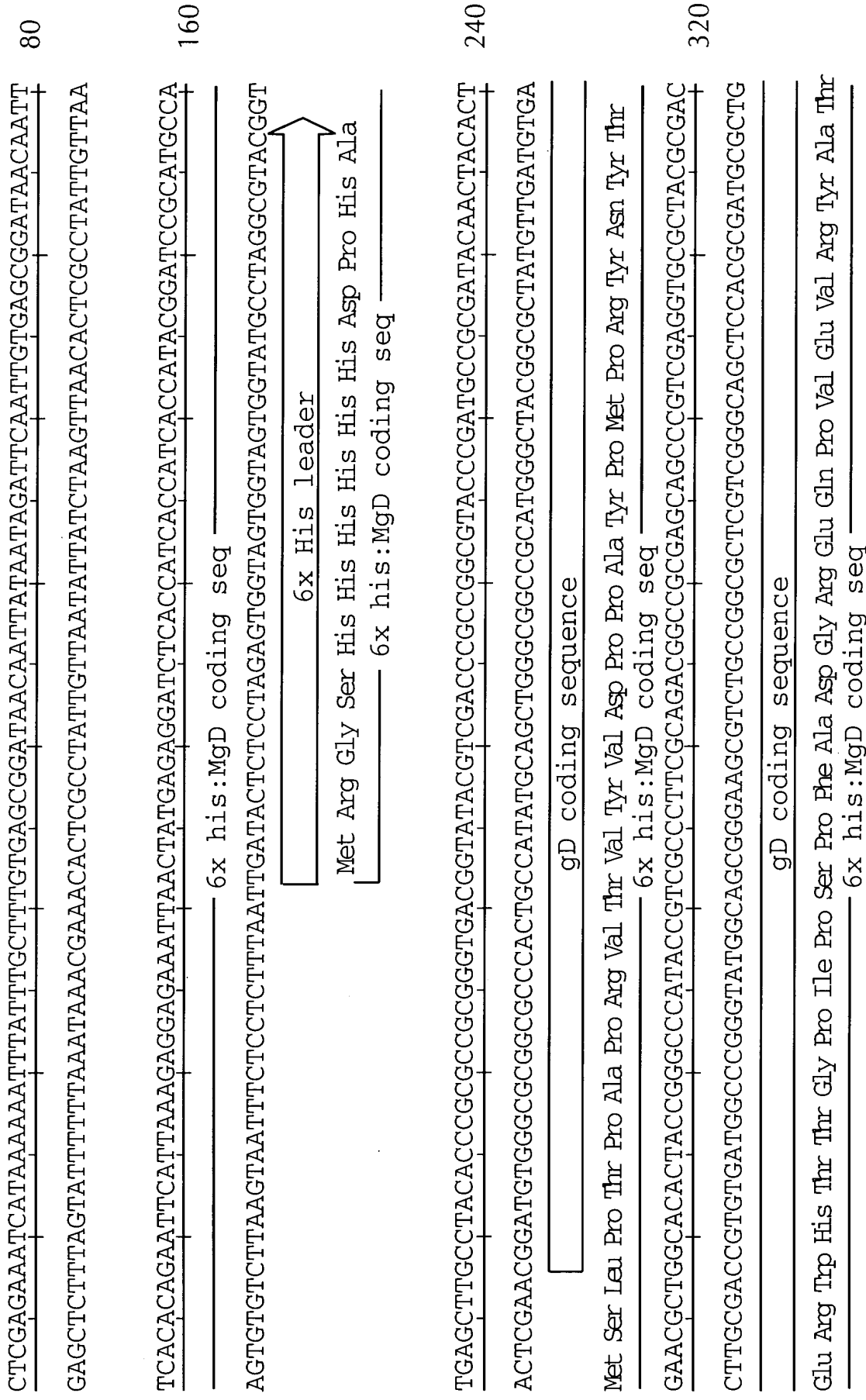


FIG. 6B

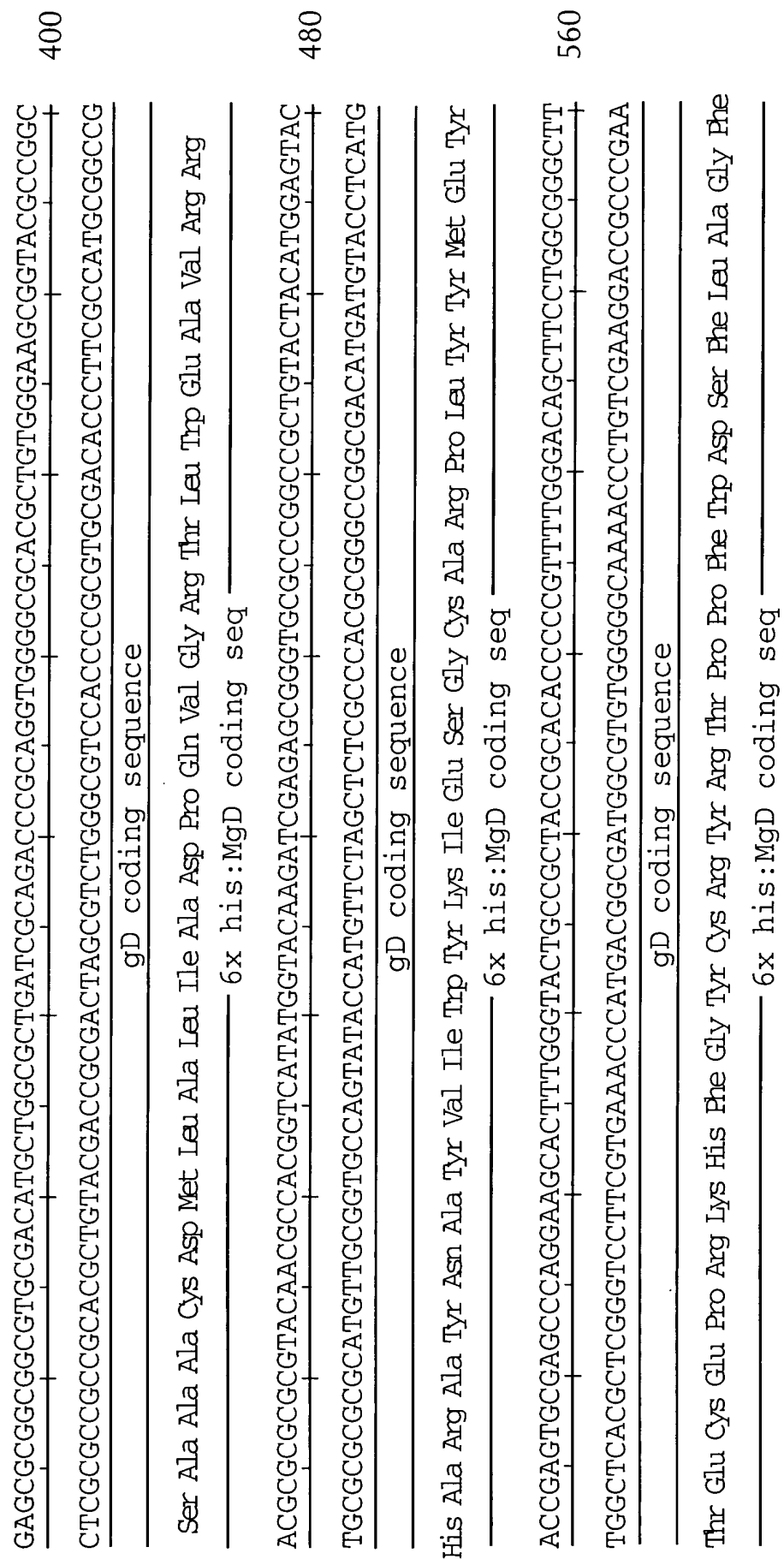


FIG. 6C

CGCTACCCACGACGAGCTGGACTGATTATGGCGGCGCCCGGGCTCGTCAGGGCCAGTACCGACGCGCGC 640

GCGATGGGTGCTGCTCGACCCCTGACTAATACCGCGCGCGCGCGAGCAGCTCCCGTCAATGGCTGCGCGCGC

gd coding sequence

Ala Tyr Pro Thr Asp Asp Glu Leu Gly Leu Ile Met Ala Ala Pro Ala Arg Leu Val Glu Gly Gln Tyr Arg Arg Ala

6x his:MgD coding seq

TGTACATCGACGGCAGGTGCGCCTATACAGATTTCATGGTTTCGCTGCCGCGGGGACTGCTGGTTCTCGAAACTCGGC

720

ACATGTAGCTGCCGTGCCGATATGTCTAAAGTACCAAGCAGCGCGCGGCCCTGACGACCAAGAGCTTTGAGCCG

gd coding sequence

Leu Tyr Ile Asp Gly Thr Val Ala Tyr Thr Asp Phe Met Val Ser Leu Pro Ala Gly Asp Cys Trp Phe Ser Lys Leu Gly

6x his:MgD coding seq

GCGGCTCGCGGTACACCTTTGGCGGTGCTTCCCGCGCGGTACGAGTACGAGCAAAAGAGTTCTGCGCCTGACGTATCT

800

CGCCGAGCGCCCATGTGGAACCGCGCACGAAGGCGCGGCCCTAATGCTCTGTTTCTTCCAAGACGCGGACTGCATAGA

gd coding sequence

Ala Ala Arg Gly Tyr Thr Phe Gly Ala Cys Phe Pro Ala Arg Asp Tyr Glu Gln Lys Lys Val Leu Arg Leu Thr Tyr Leu

6x his:MgD coding seq

CACGCAGTACTACCCGCAGGAGGCACACAAGGCCATAGTCGACTACTGGTTTCATGCGCCACGGGGCGTCTCCGCCGT

880

GTGCGTCATGATGGGCGTCCCTCCGTGTTCGGGTATCAGCTGATGACCAAGTACGCGGTGCCCCCGCAGCAAGGCGGCA

gd coding sequence

Thr Gln Tyr Tyr Pro Gln Glu Ala His Lys Ala Ile Val Asp Tyr Trp Phe Met Arg His Gly Val Val Pro Pro

6x his:MgD coding seq

ATTTTGAGGAGTCGAAGGCTACGAGCCCGCCTGCGCCGATGGGGTTCCCCCGCCACCCGCGCAGCAGGAGGCC

960

TAAAACTCCTCAGCTTCCCGATGCTCGGCGGGGACGGGGTACCCCCAAGGGGCGGTGGGCCGCTGCTGCTCCGG

gd coding sequence

Tyr Phe Glu Glu Ser Lys Gly Tyr Glu Pro Pro Pro Ala Ala Asp Gly Gly Ser Pro Ala Pro Pro Gly Asp Asp Glu Ala

6x his:MgD coding seq

FIG. 6D

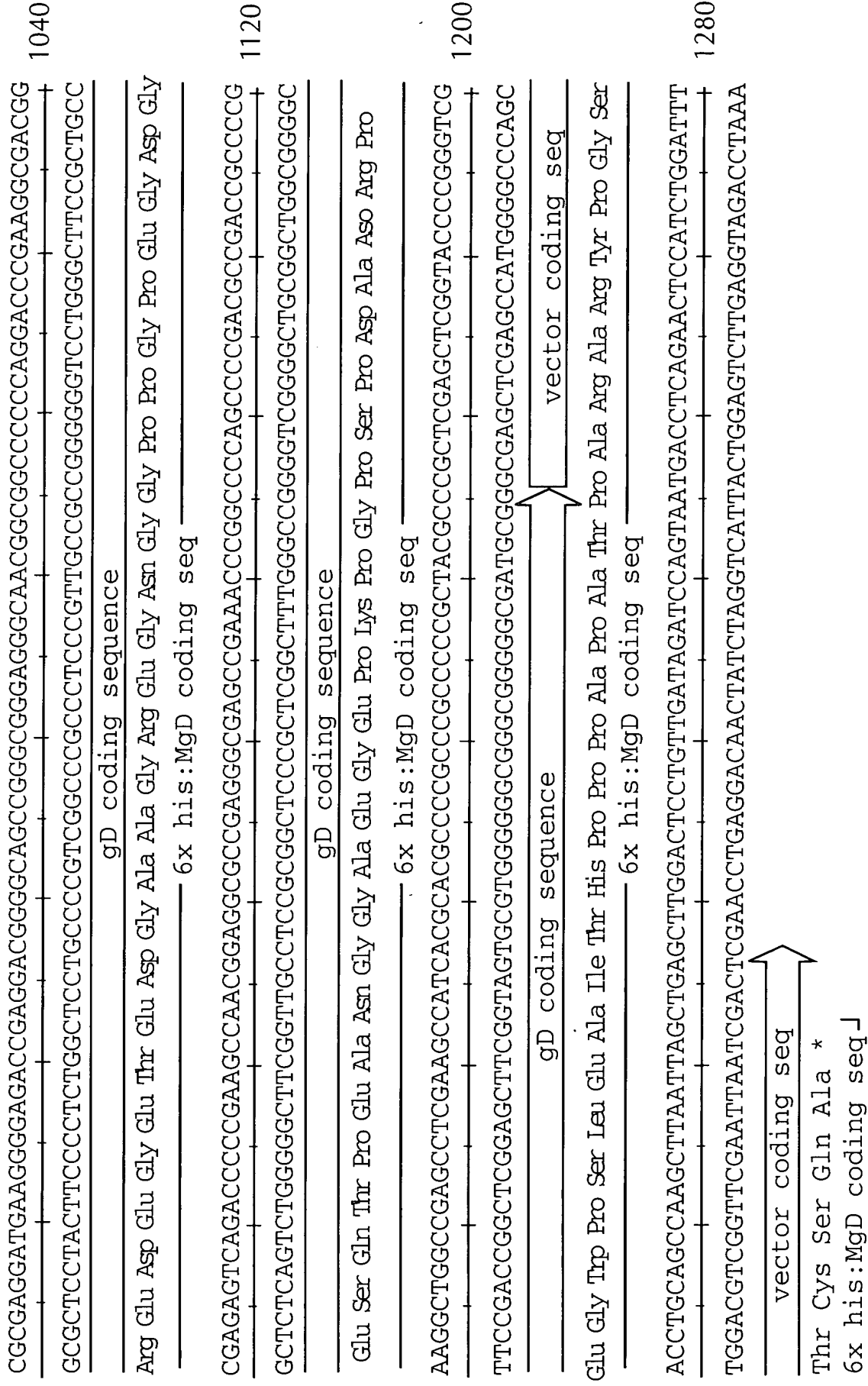


FIG. 7A

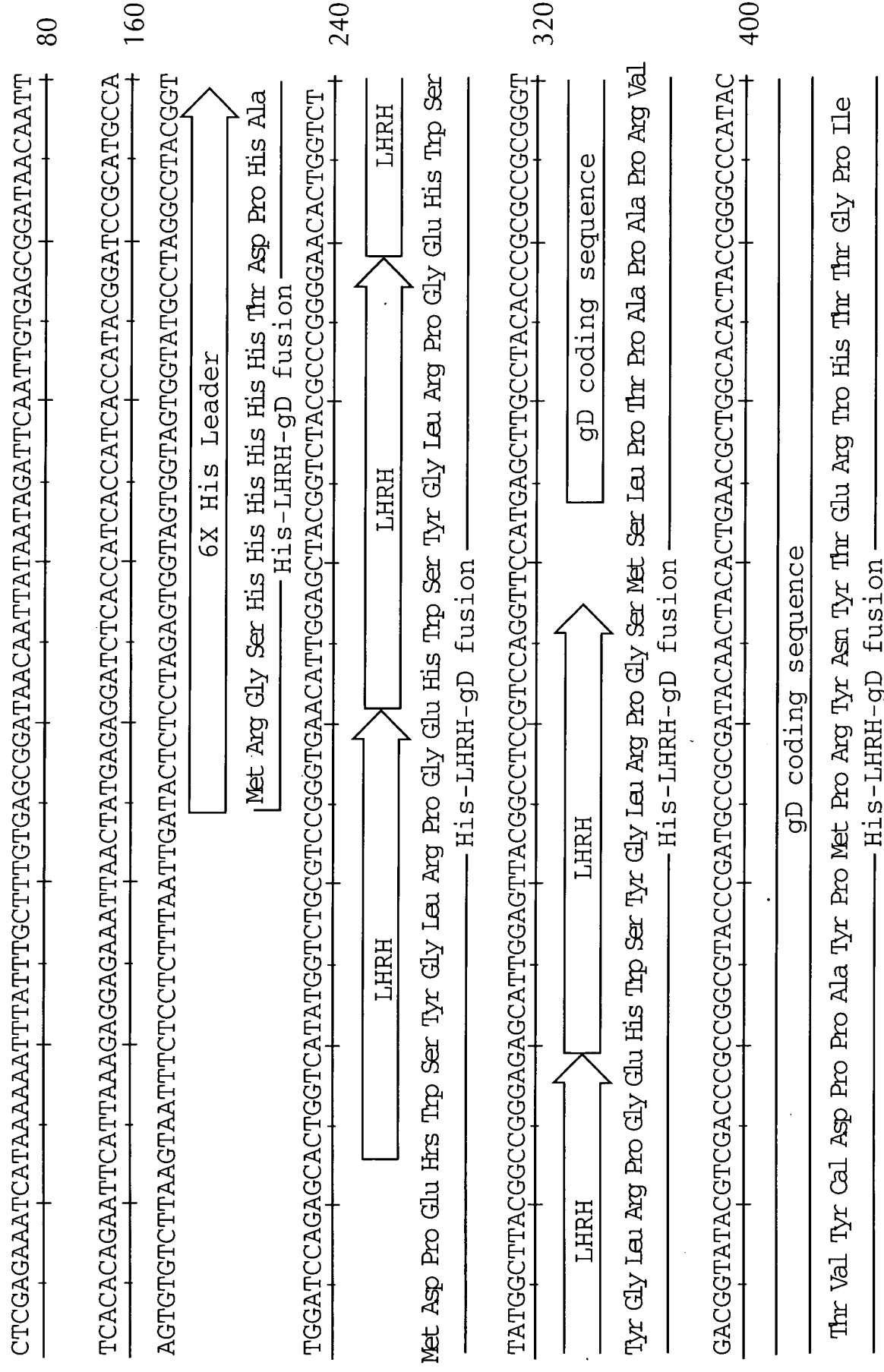


FIG. 7B

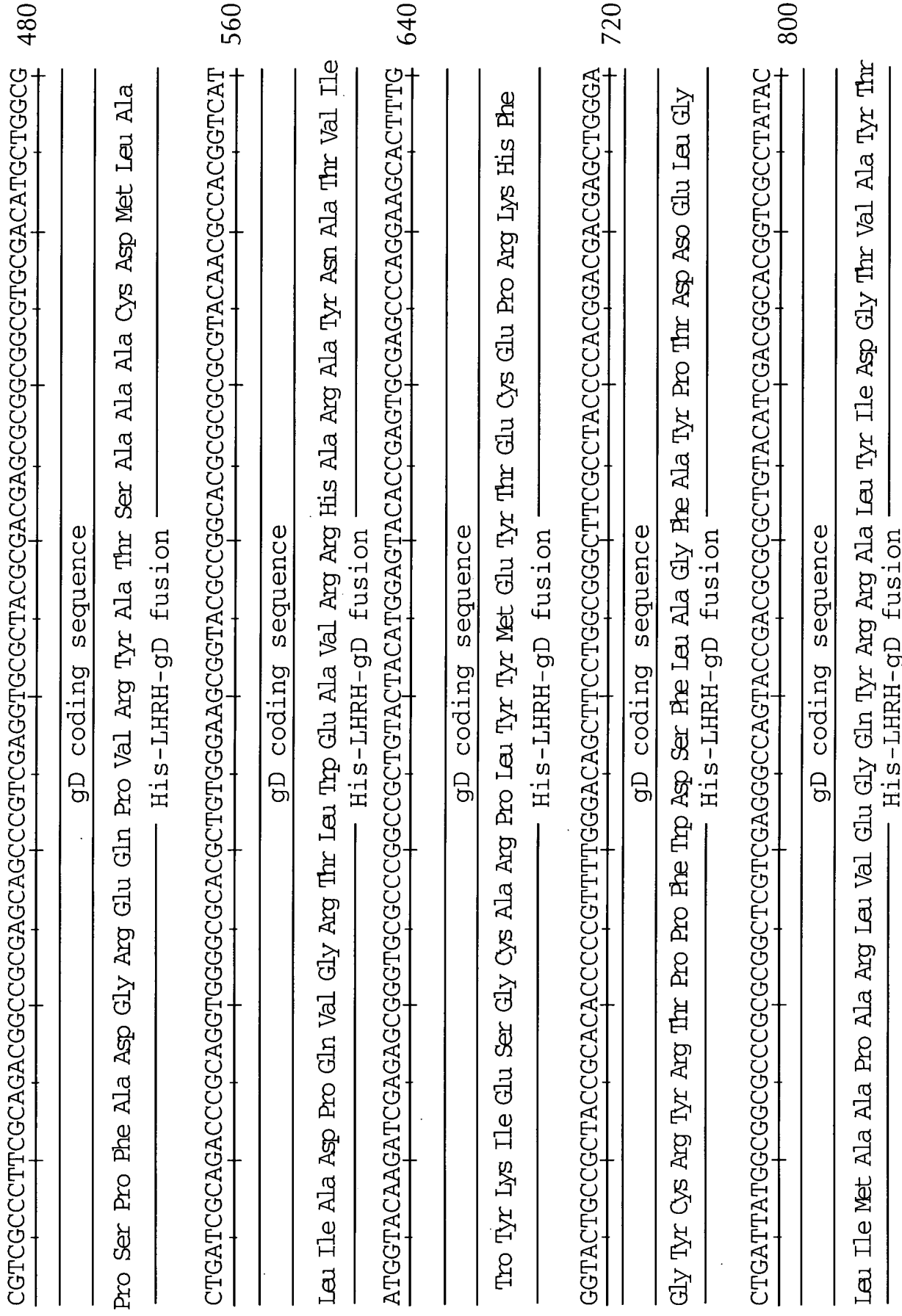


FIG. 7C

AGATTTCATGGTTTCGCTGCCGGCCGGGACTGCTGGTTCTCTCGAAACTCGGGCGGGCTCGGGGTACACCTTTGGCGCGT	880
gD coding sequence	
Asp Phe Met Val Ser Leu Pro Ala Gly Asp Cys Trp Phe Ser Lys Leu Gly Ala Ala Arg Gly Tyr Thr Phe Gly Ala	
His-LHRH-gD fusion	
GCTTCCCCGGCCGGGATTACGAGCAAAAGAGTTCTGCGCCTGACGTATCTCAGCGAGTACTACCCGAGGAGGCACAC	960
gD coding sequence	
Cys Phe Pro Ala Arg Asp Tyr Gly Gln Lys Lys Val Leu Arg Leu Thr Tyr Gln Tyr Pro Gln Glu Ala His	
His-LHRH-gD fusion	
AAGGCCATAGTCGACTACTGGTTTCATGCGGCCACGGGGCGTCGTTCCGCCGTATTTTGAGGAGTCTGAAGGGCTACGAGCC	1040
gD coding sequence	
Lys Ala Ile Val Asp Tyr Trp Phe Met Arg His Gly Gly Val Val Pro Pro Tyr Phe Glu Glu Ser Lys Gly Tyr Glu Pro	
His-LHRH-gD fusion	
GCCGCCCTGCCCGCATGGGGTTCCCCCGCCACCCCGCGACGACGAGGCCCGGAGGATGAAGGGGAGACCGAGGACG	1120
gD coding sequence	
Pro Pro Ala Ala Asp Gly Gly Ser Pro Ala Pro Pro Gly Asp Asp Glu Ala Arg Glu Asp Glu Gly Thr Glu Asp	
His-LHRH-gD fusion	
GGGCAGCCGGGGGAGGGCAACGGCGGCCCGCCCGGACCCGAGGACCGGAGAGTCAAGACCCCGAAGCCCAACGGA	1200
gD coding sequence	
Gly Ala Ala Gly Arg Glu Gly Asn Gly Gly Pro Pro Gly Pro Glu Gly Asp Gly Glu Ser Gln Thr Pro Glu Ala Asn Gly	
His-LHRH-gD fusion	

FIG. 7D

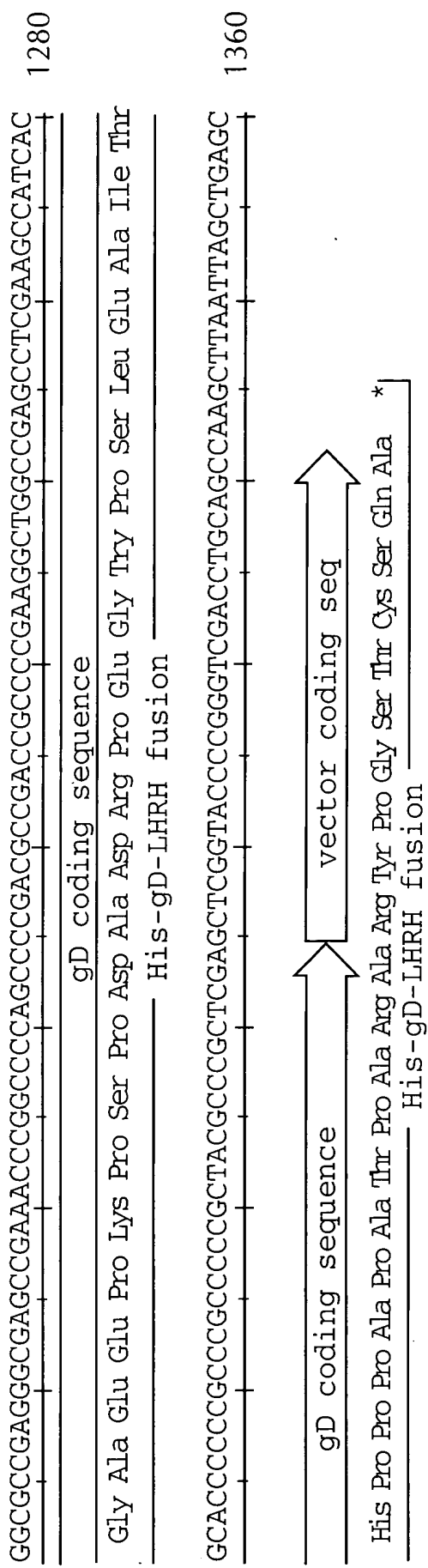


FIG. 8A

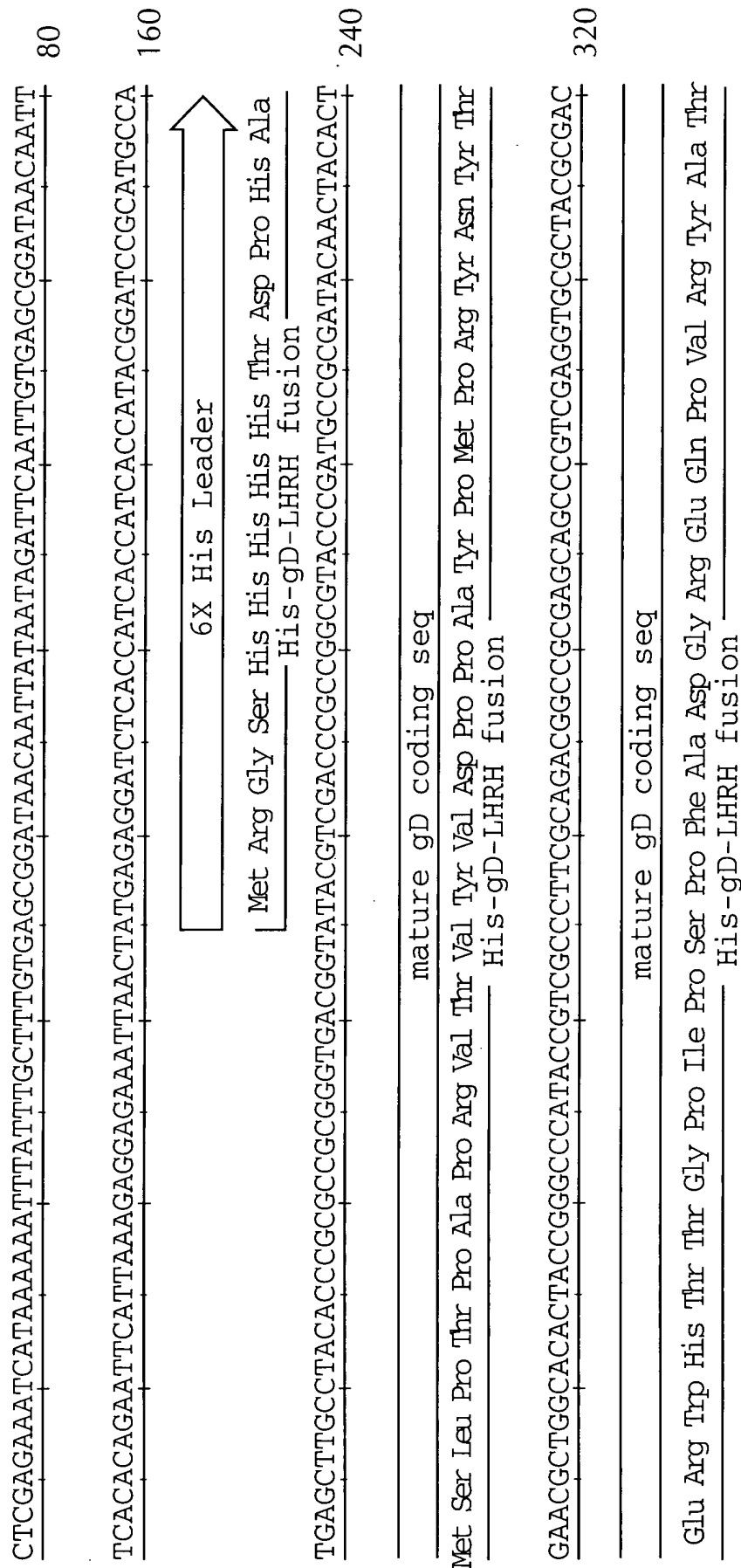


FIG. 8B

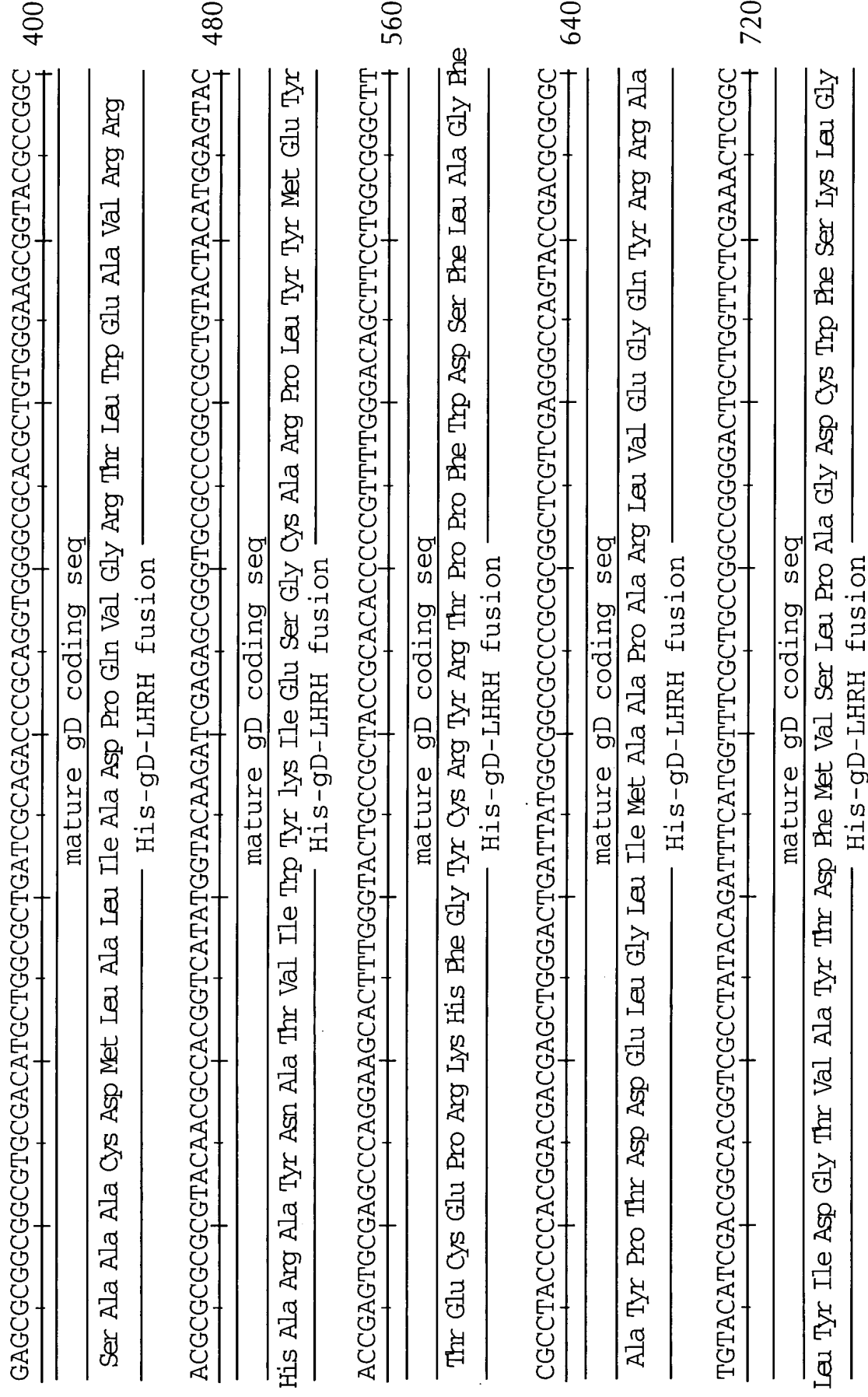


FIG. 8C

CGGGCTCGCGGTACACCTTTGGCGCGTGTCTTCCCGGCCCGGGATTACGAGCAAAAGAGTTCTGCGCCTGACGTATCT 800

mature gD coding seq

Ala Ala Arg Gly Tyr Thr Phe Gly Ala Cys Phe Pro Ala Arg Asp Tyr Glu Gln Lys Lys Val Leu Arg Leu Thr Tyr Leu
His-gD-LHRH fusion

CACGCACTACTACCCGAGGAGCACACAAGGCCATAGTCGACTACTGGTTCATGCGCCACGGGGCGTCTGTTCCGCCGT 880

mature gD coding seq

Thr Gln Tyr Tyr Pro Gln Glu Ala His Lys Ala Ile Val Asp Tyr Trp Phe Met Arg His Gly Val Val Pro Pro
His-gD-LHRH fusion

ATTTTGAGGAGTCGAAGGGCTACGAGCCGCGCCCTGCGCGCGATGGGGGTTCCCCCGCGCCACCCGGCGACGACGAGGCC 960

mature gD coding seq

Tyr Phe Glu Glu Ser Lys Gly Tyr Glu Pro Pro Ala Ala Asp Gly Gly Ser Pro Ala Pro Pro Gly Asp Asp Glu Ala
His-gD-LHRH fusion

CGCGAGGATGAAGGGGAGACCGAGGACCGGGGAGCCGGCGGGAGGGCAACGGCGGCCCCCGAGACCCGAAAGGCGACGG 1040

mature gD coding seq

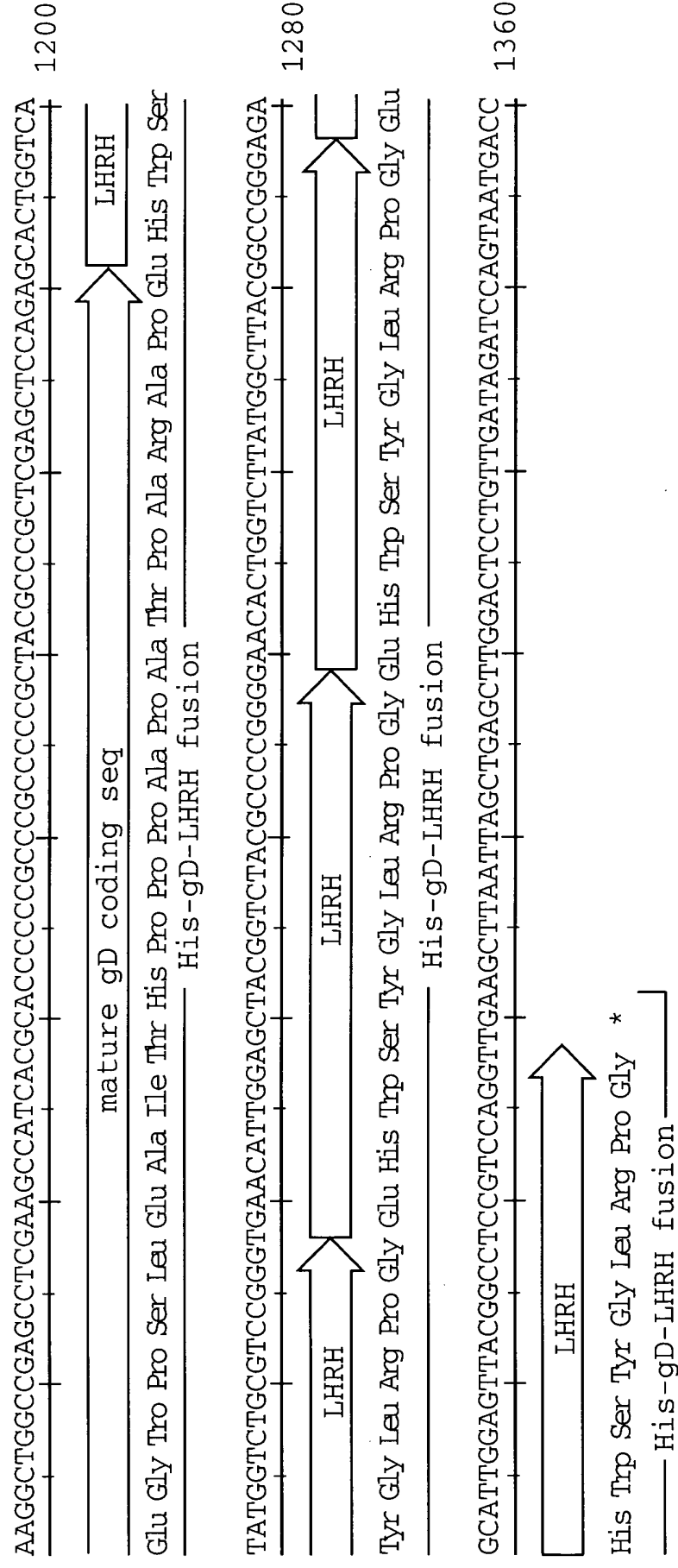
Arg Glu Asp Glu Gly Glu Thr Glu Asp Gly Ala Ala Gly Arg Glu Gly Asn Gly Gly Pro Gly Pro Glu Gly Asp Gly
His-gD-LHRH fusion

CGAGAGTCAGACCCCGAAGCCAAACGGAGGCGCGGAGCGGAGCCGAAACCGGGCCCCAGCCCCGACGCCGACCGCCCCC 1120

mature gD coding seq

Glu Ser Gln Thr Pro Glu Ala Asn Gly Gly Ala Glu Gly Glu Pro Lys Pro Gly Pro Ser Pro Asp Ala Asp Arg Pro
His-gD-LHRH fusion

FIG. 8D



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FIG. 9B

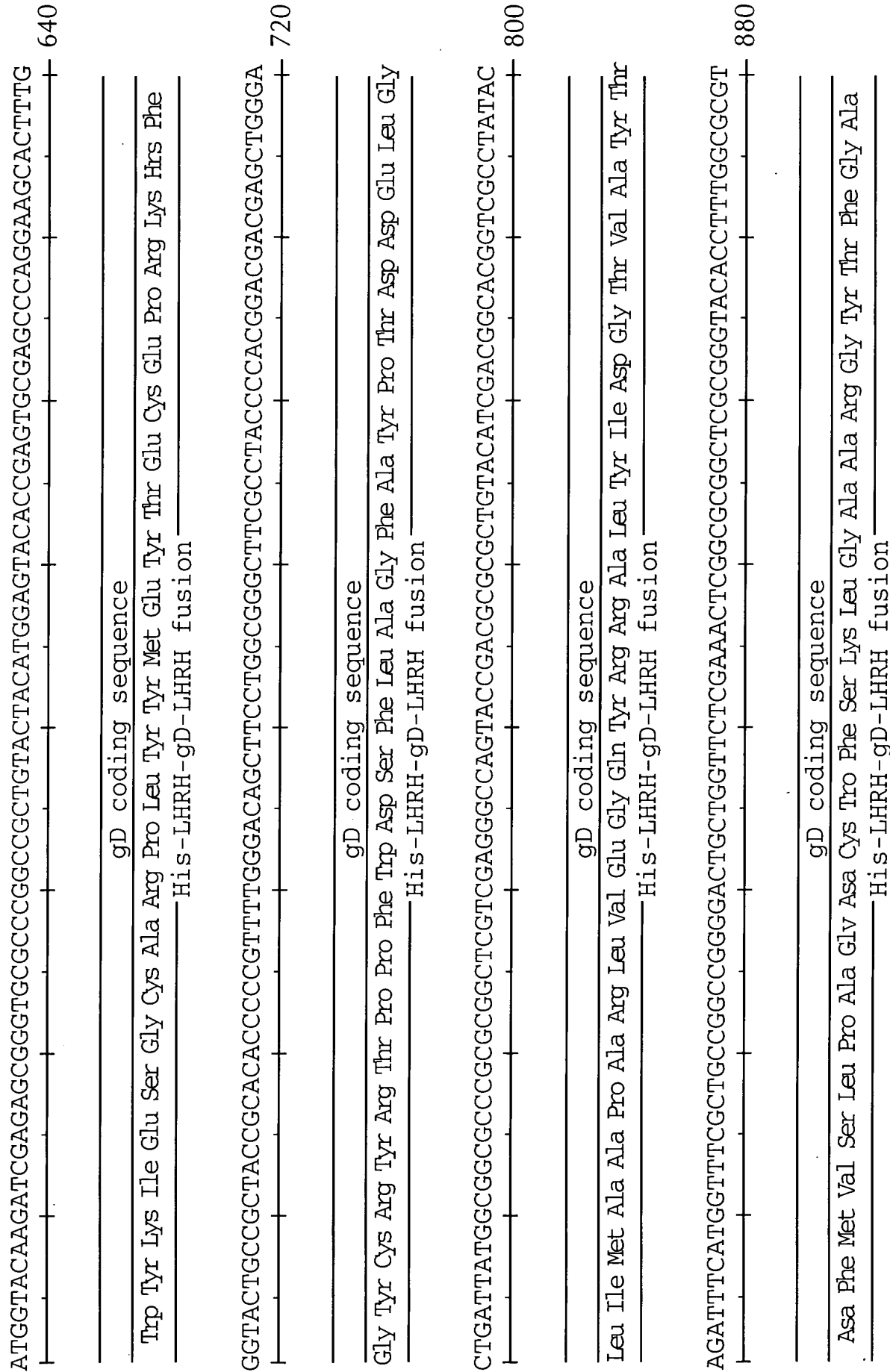


FIG. 9C

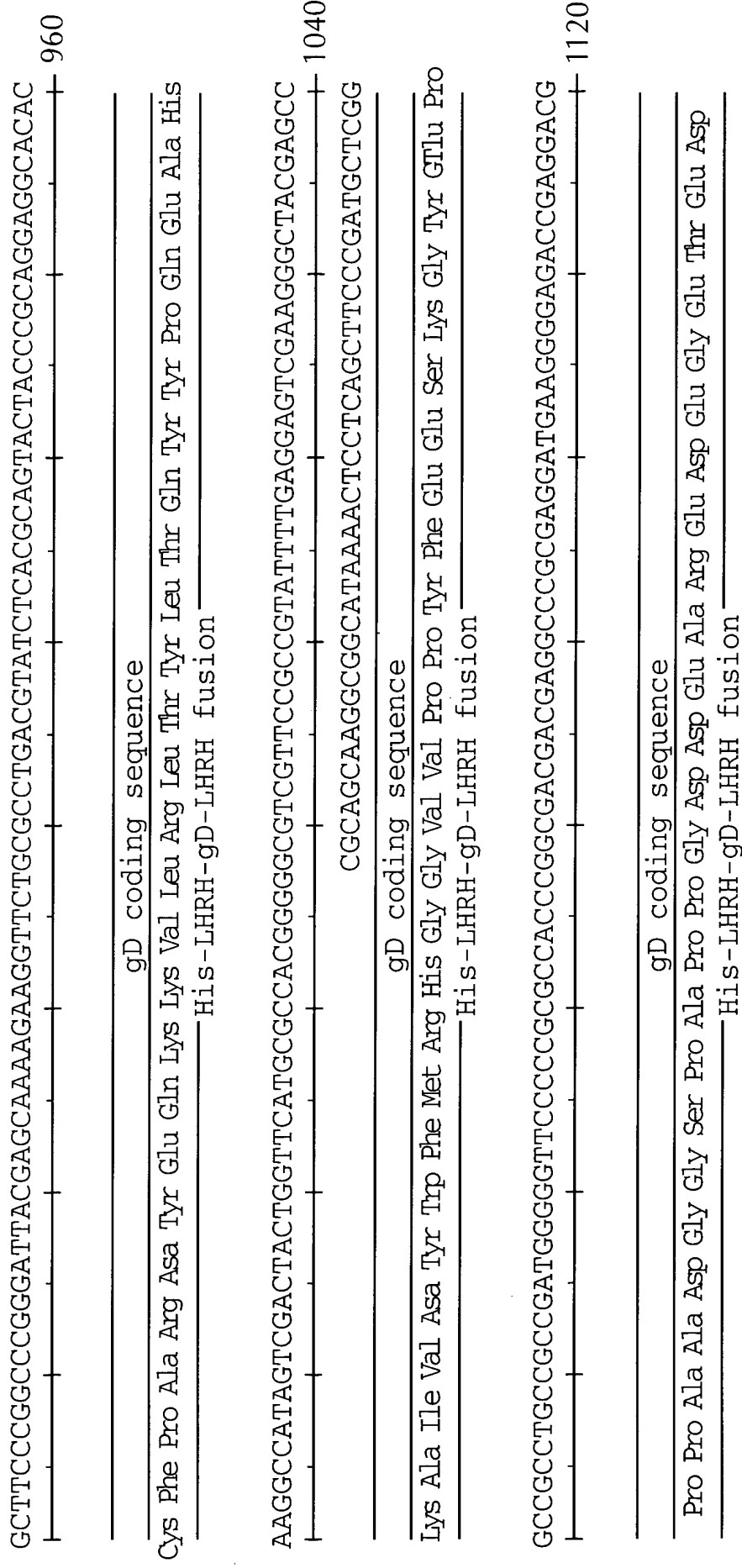


FIG. 9D

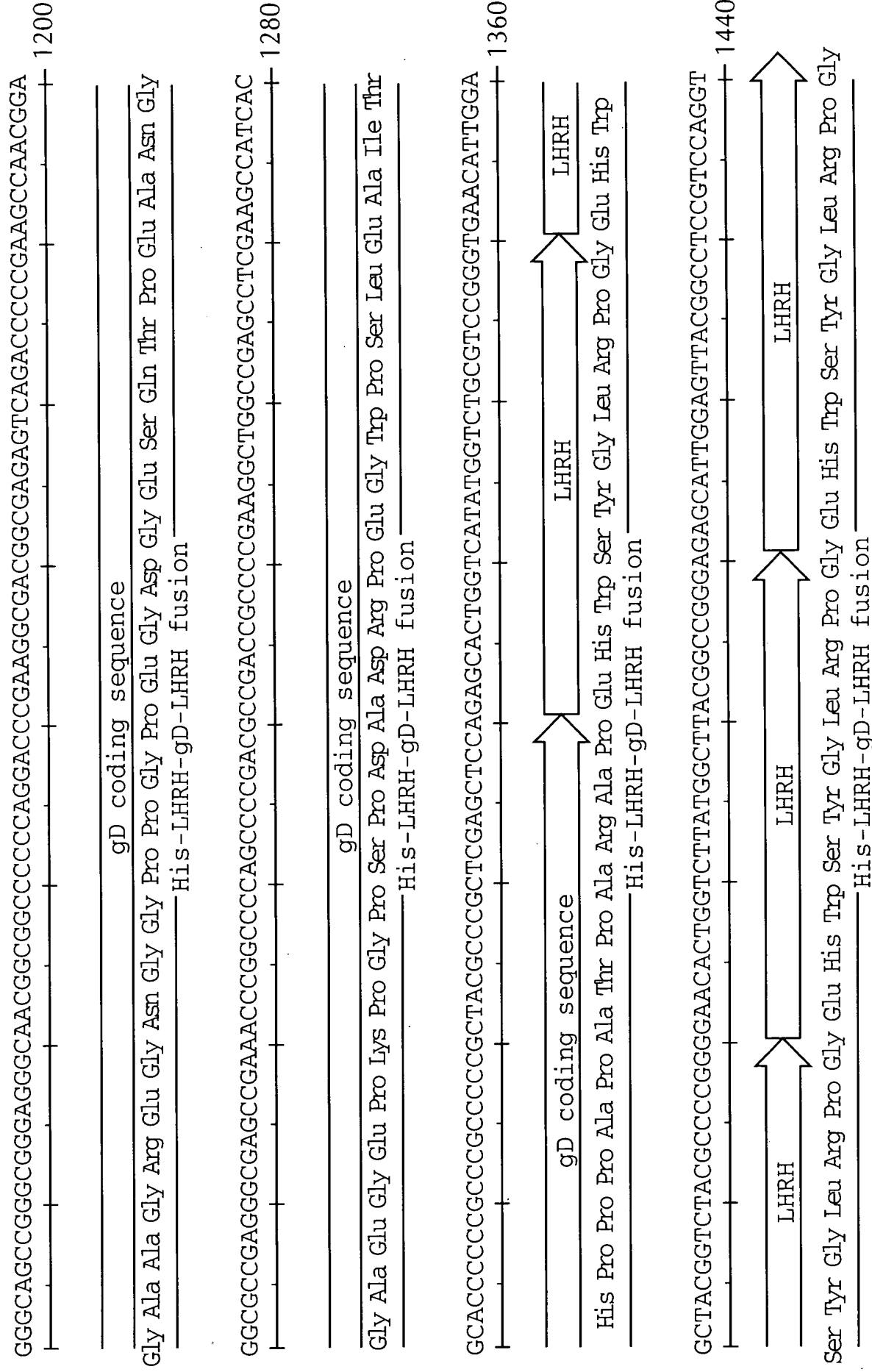


FIG. 10

A: pQE_gD
B: pQE_gD-LHRH
C: pQE_LHRH-gD
D: pQE_LHRH-gD-LHRH

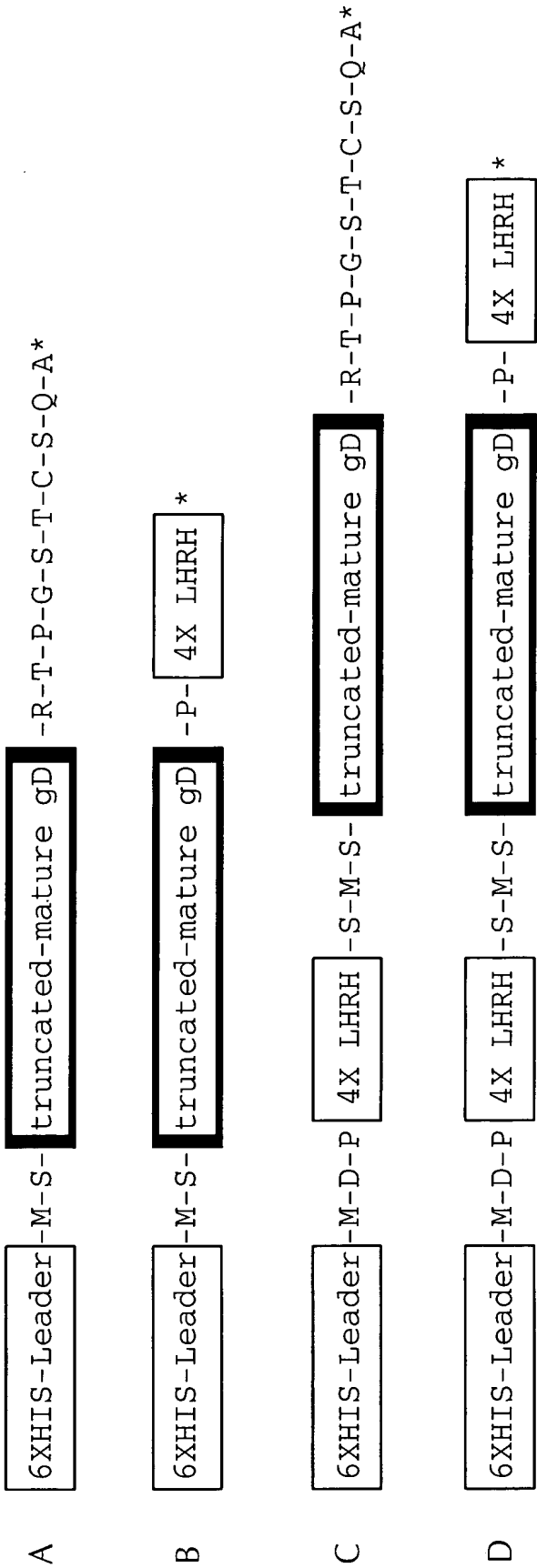
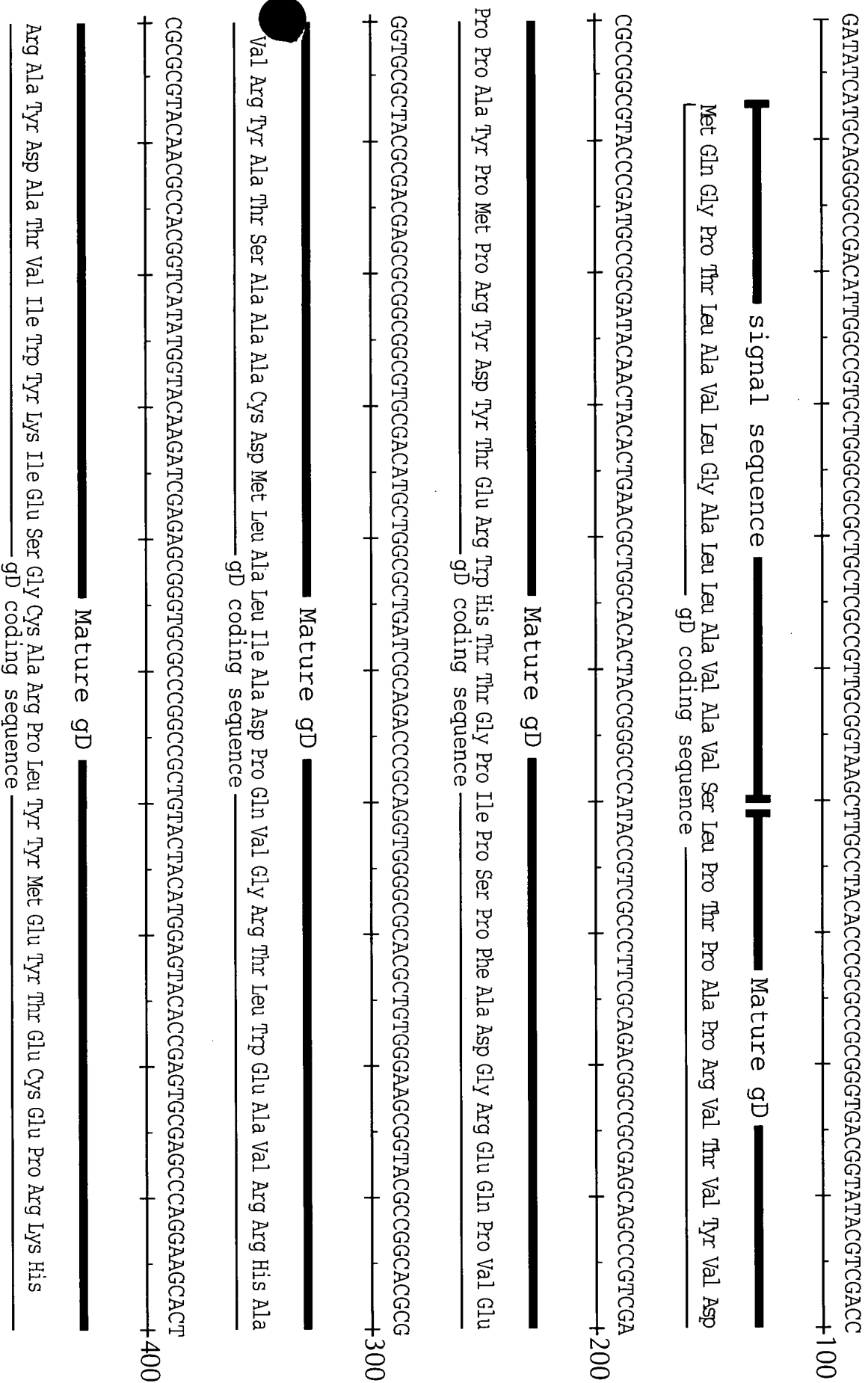


FIG. 11A



-500

1. The first step in the process is to identify the problem or issue that needs to be addressed. This involves gathering information and understanding the context of the problem.

gd coding sequence _____
 Phe Leu Ala Gly Phe Ala Tyr Phe Ile Asp Asp Glu Leu Gly Leu Ile Met Ala Ala Phe

CGACGGCCGGCCCTGACGACC

1000

gd coding sequence

-700

[REDACTED]

gd coding sequence

008+

1000

gd coding sequence

-1000

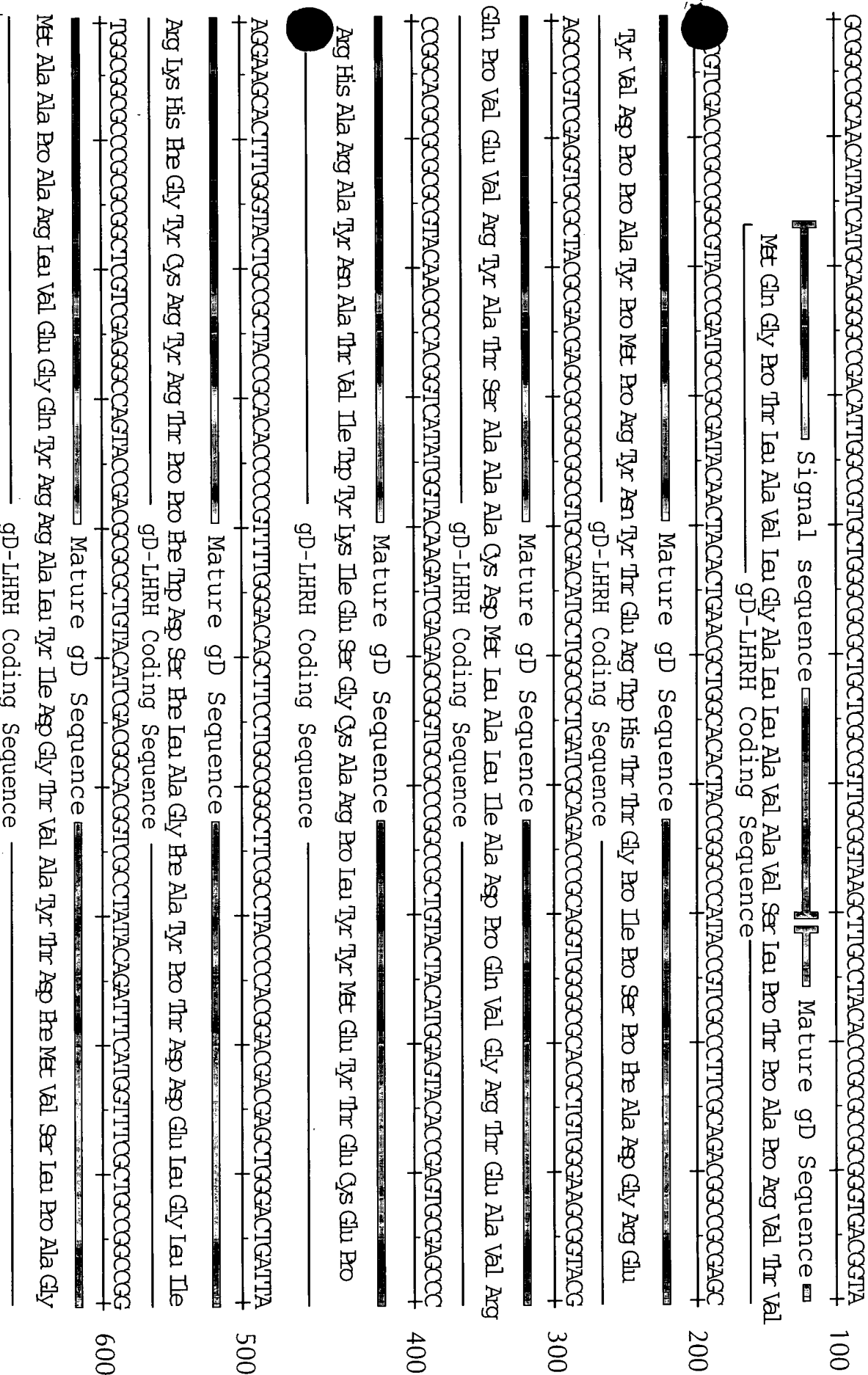
Mature gD

1080

Mature gD

+

FIG. 12A



+

